A LINE BY TESTER ANALYSIS OF CHROMOSOME SUBSTITUTION LINES IN COTTON

A Thesis

by

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ABSTRACT

Conventional breeding techniques have been minimally successful in introgressing novel fiber quality traits of *Gossypium barbadense* L. into elite *G. hirsutum* L. cultivars. The Cotton Improvement Lab at Texas A&M AgriLife Research utilized Chromosome Substitution Lines (CSLs) to address the recalcitrant nature of the *G. barbadense* fiber traits. Sixteen CSLs, each having only one *G. hirsutum* chromosome replaced with a *barbadense* chromosome, were used in a Line by Tester (lxt) design to evaluate combining ability for fiber upper half mean length (UHML), strength (Str), Lint % (lint wt./seedcotton wt.*100), and Scwt yield (Seedcotton weight). Three upland testers were used, including an extra-long staple type, TAM 182-33, an extra strength upland type, TAM 06WE-621, and a high-yield cultivar, Tamcot 73. Fiber properties of parents and F_1s developed by crossing each CSL with each tester were assessed by High Volume Instrument (HVI).

Combining ability analysis of the HVI and yield data indicated CS-B25, CS-B18, CS-B02 and CS-B11sh as good general combiners for UHML, Str, Lint % and Scwt yield, respectively. Tamcot 73/CS-B01 was a good specific combiner for UHML and Scwt yield among all F_1s. The F_1s showed additive gene action for UHML, Str, Lint %, whereas yield displayed a dominance gene effect. The results indicate CSL potential in unlocking the beneficial alleles in *G. barbadense* and aid in the stable introgression of its superior fiber quality into *G. hirsutum* species.

DEDICATION

I would like to dedicate this thesis to my family and friends. I would like to thank my parents and my brother for their support and encouragement throughout my research tenure. I would also like to thank my grandparents for their love and guidance in my life.

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NOMENCLATURE

c –	Crosses
CSL –	Chromosome Substitution Lines
Elon-	Elongation
ELSU –	Extra Long Staple Upland
ESU-	Extra Strength Upland
g –	Genotypes
GCA –	General Combining Ability
HVI –	High Volume Instrument
l –	Line
LxT –	Line x Tester Interaction
Mic –	Micronaire
MP-	Mid-Parent
MSE –	Mean Square of Error
p –	Parents
p vs. c –	Parents vs. Crosses
S.E. –	Standard Error
SCA –	Specific Combining Ability
Scwt	Seedcotton weight
Str –	Strength
t –	Tester
U.S. –	United States of America

UHML – Upper Half Mean Length

UI – Uniformity Index

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CHAPTER I

INTRODUCTION

Cotton (*Gossypium* spp.) is the most widely used fiber crop relative to the global textile industry. While four species of cotton are cultivated, two A-genome diploid (2n=2x=26) and two AD-genome tetraploid (2n=4x=52) species, one of the latter, *G. hirsutum* (L.), dominates contemporary production.

Fiber traits such as length, strength, length uniformity index, elongation before break, etc., predict how well cotton fibers may function in the production of yarns and fabric. Competition from synthetic fibers and new spinning technologies are requiring producers to grow stronger, longer and finer cotton fibers. A comprehensive genetic approach provides cotton breeders with tools that improve efficiency of phenotypic selection for the improvement of traits such as fiber length, strength, lint %, and lint yield. Advances in spinning technologies, such as air jet spinning, which can produce yarn at a faster rate (Eldessouki et al., 2015), requires longer fibers with higher strength and fineness. Moreover, increased competition from synthetic fibers with competitive spinning properties have accentuated the need to enhance cotton fiber properties through breeding.

Improvements in fiber properties are feasible only if new genetic combinations can be derived. However, several lines of evidence show relatively low genetic diversity, especially among elite cotton cultivars and germplasm. The breeding methods and parental material employed in the last few decades have resulted in a slowing of

genetic gain or narrowing of the genetic base in upland cotton (Kuruparthy and Bowman, 2013). Chromosome substitution may be one genetic manipulation technique that can lead to the improvement of fiber traits by allowing breeders to introgress a limited number of *G. barbadense* alleles and add new genetic diversity into elite upland *G. hirsutum* germplasm. To create interspecific chromosome substitutions in cotton, one chromosome of the *G. hirsutum* recurrent parent (maternal) is replaced with one chromosome from the other species, e.g., *G. barbadense*, donor parent (paternal). Once rendered homozygous, chromosome substitution lines are sometimes alluded to as disomic alien chromosome substitutions or simply disomic substitutions. Since upland cotton has 26 pairs of chromosomes, a complete set of chromosome substitution lines (CSL) for a given donor species would consist of 26 lines, each differing by a specific non-*hirsutum* chromosome.

Two species, *G. barbadense* ($[AD]_2$ genome) and *G. hirsutum* ($[AD]_1$ genome), were used to study the association of agronomic traits with specific chromosomes, based on relative effects of specific CSL. These two 52-chromosome *Gossypium* species are regarded as AD-genome allotetraploids with 26 pairs of chromosomes, including 13 pairs of A and 13 pairs of D chromosomes. Stelly et al. (2005) developed and released 17 CSL from a doubled-haploid *G. barbadense* donor line (3-79) to create a CS-B line series. These lines were created through hypoaneuploid-based backcrossing to hypoaneuploids that had genetic backgrounds nearly isogenic to *G. hirsutum* line Texas Marker-1 (TM-1), a highly inbred line of Deltapine 14 that has been used in numerous genetic studies, thus being well characterized. The paternal donor line, 3-79, is a highly

inbred (doubled haploid) accession of *G. barbadense*. Pima (*G. barbadense*), also referred as Extra Long Staple (ELS) cotton, exhibits an UHML of 1.38 inches or longer as compared with medium staple upland cultivars (*G. hirsutum*) that exhibit UHML ranging from 1.06 to 1.14 inches (http://www.cottoninc.com/fiber/quality). However, Pima cultivars are lower yielding than upland cultivars in the majority of the cotton producing regions of the world and make up only about 10% of global cotton hectarage. (Smith et al., 2008).

Jenkins et al. (2012) looked at the genetic effects of the CSL when crossed with elite, commercial upland cultivars for the improvement of fiber quality and yield. The aim of the study was to find favorable alleles in the CSL that can be used for introgression into cultivars. Interspecific crosses, previously studied, have been unsuccessful in stable introgression of Pima fiber quality into upland elite germplasm (Beasley and Brown 1942; McKenzie, 1970). If genes for any of the superior fiber quality traits of Pima are confined to specific chromosomes, then the CSL could provide a breeding tool to introgress those alleles into upland without introducing potentially undesirable Pima alleles found on the other 25 chromosomes. Chromosome-specific QTL for these traits could lead to the development of markers for fiber quality traits which could further aid breeders in their selection processes.

CHAPTER II

REVIEW OF LITERATURE

Measuring Cotton Fiber Quality

The classification of cotton is based on parameters of length, uniformity, strength, micronaire, leaf and color grade, and trash (Cotton Incorporated, 2015). Fiber quality is determined by genotype, the environment in which the genotype is grown, and their interaction. Fiber quality parameters are affected by weather conditions, type of harvesting machine, and ginning method (Anthony, 1999). Apart from yield, fiber quality adds monetary value to the bale of cotton for the producer. Classical breeding techniques and methodologies have resulted in significant fiber quality improvement (Culp, 1992; Cooper, 1992; Gannaway and Dever, 1992; Elzik and Thaxton, 1992; Smith, 1992). Rapid and more efficient improvements in fiber spinning technologies, such as air jet spinning, which is more cost effective and faster (Basu and Oxenham, 1999), and the competition from improved synthetic fibers have increased the need for breeders to improve cotton fiber quality.

High Volume Instrument

Fiber quality is determined by using High Volume Instrument (HVI) technology; a technology adopted by the U.S. Department of Agriculture in 1969 and is required on every bale of cotton marketed in the United States (U.S.) (Hsieh, 1999; Ramey, 1999). It is the preferred method of measurement due to its speed and efficiency. HVI uses

automated sampling techniques and measures a high volume of fiber bundles (Kelly et al., 2012). It uses a fibrosampler in which a beard of fibers is created with fibers parallel to each other (Hertel, 1940) and is then optically scanned for measurements (Ramey, 1999). The fibrogram methods is the basis for determining UHML (Ramey, 1999; Cui et al., 2009) and can be programmed to provide staple length in 1/32nd inch increments. Staple length, another name for UHML, is recognized as the criteria for length when determining the price of a bale of cotton. Along with UHML, Str, and micronaire are used also in assessing the economic premiums or discounts. HVI measures five fiber parameters: micronaire, UHML, UI, Str, and elongation of fibers before rupture (elon).

Upper Half Mean Length

UHML is the average length of the longest half of fibers in a sample (Ramey, 1999). It is accepted widely as the standard in determining cotton length (Smith et al., 2009), though there is a recognition of its variances in measuring fibers less than 0.5 of an inch in length (Cui et al., 2007; Cai et al., 2010). Upland cotton is classified into four categories based on UHML: short (≤.827 in), medium (.867–.984 inches), medium-long (1.02–1.10 inches), and long (1.14–1.33 inches). With the recent development of extra-long staple upland (ELSU) by Texas A&M AgriLife Research, a fifth class may be necessary. Pima UHML is divided into long (1.14–1.33 inches) and extra-long (>1.33 inches) (Bradow and Davidonis, 2000). ELSU genotypes exhibit an UHML more than 1.33 inches, values equal to Pima cultivars (Smith et al., 2009).

Fiber Bundle Strength

HVI uses the clamped beard of fibers, derived from a sample volume, for determining strength (Taylor, 1986). Str is recorded at the point when the applied force ruptures the beard. Since the beard is clamped on both sides, the strength measurement is made from the average of the two sides. Str is measured as tenacity, i.e., g tex^{-1}, and is calculated from the force to break divided by the bundle mass (Ramey, 1999). The breaking load is the mass in grams, whereas tex refers to the linear density in g km^{-1} (Munro, 1987; Taylor, 1994). Fiber strength is categorized into five categories: weak (23 g tex^{-1} and below), intermediate (24-25 g tex^{-1}), average (26-28 g tex^{-1}), strong (29-30 g tex^{-1}), and very strong (31 g tex^{-1} and above), (Ramey, 1999)

Interspecific Hybridization: *G. barbadense* x *G. hirsutum*

Referred to as the New World cotton species, *Gossypium barbadense spp.* and *Gossypium hirsutum spp*, have always been of key interest to breeders exploring the AD genome for trait introgression. They are the only two cultivated species in the U.S., where *hirsutum* cultivars account for 97% of cotton production and *barbadense* for 3% (USDA-NASS, 2016). *G. barbadense* L. cultivars, Pima and Sea Island biotypes, have long been considered for introgression of its superior fiber quality into upland elite cultivars (Schwartz and Smith, 2008). Pima Cotton has a longer growing season and requires a stable climate, thereby being restricted to a relatively small hectareage (Saha et al., 2010).

The genetic diversity in upland cotton is narrow because of the bottleneck effect over the decades due to polyploidization, domestication, and continuous selection (Hulse-Kemp et al., 2014). Conventional breeding techniques and methods generally have been unsuccessful in introgressing the fiber quality traits of *G. barbadense* into *G. hirsutum*. Genetic incompatibility, inverse relationship among traits, infertility, and distorted segregation are some factors that have led to these difficulties (Saha et al., 2004). Interspecific hybrids generally are late maturing and contain a high amount of motes, making it unsuitable for production in the cotton belt (Zhang et al., 2014)

Chromosome Substitution Lines

Each highly backcrossed interspecific substitution line ideally contains a single chromosome or chromosome segment from the donor species. When the recurrent parent is monotelodisomic (missing the most of one chromosome arm) rather than monosomic (missing one entire chromosome), most or all of the chromosome arm of 3-79 (*G. barbadense*), is substituted into a near-isogenic background of TM-1 (*G. hirsutum*) for the development of CSL in cotton (Stelly et al., 2005). 'Lo' and 'sh' are used to designate a long arm and short arm, respectively, for a specific chromosome (Stelly et al., 2005). The procedure and the development of CSL is described by Stelly et al. (2005). Each interspecific substitution line is expectedly isogenic to the recurrent parent, but in reality, the degree of isogenicity depends on the degree of backcrossing, homozygosity of the recurrent parent and other factors. If the recurrent parents are isogenic to each other and a common parent, then the respectively derived CSLs will be

isogenic to each other and their common parent. In cotton, the primary monosomics and monotelodisomics were backcrossed into the inbred TM-1, such that most of the CS-B lines are isogenic. However, CS-B lines involving two chromosomal segments, e.g., CS-B(12-19), while Upland cotton, are not necessarily isogenic to TM-1 because the recurrent parents were not isogenic to TM-1.

Chromosome substitution lines have been successfully developed in wheat (Knott, 1987); however, understanding the effects of CSL in cotton is still in its nascent stage. Saha et al. (2004) evaluated chromosome substitution lines (CS-B) for any traits that differ positively and negatively from its parents, TM-1 and 3-79. They evaluated the effects of a gene on a specific substituted chromosome and/or epistasis between the parental and CS-B genes. Some of the phenotypic mean values for agronomic traits exhibited a competitive value when compared with its parents. CS-B15sh exhibited an overall higher yield (kg ha^{-1}) than all other lines, including TM1 and 3-79. CS-B06 gave a higher lint yield than any other strain in the experiment (Saha et al., 2004).

CSL were analyzed for lint yield and three components (boll number, boll weight, and lint %) on the basis of the conditional additive-dominance (AD) genetic model (Wu et al., 2008). This study indicated a greater association of boll number with lint yield as compared with boll weight and lint percentage. An ADAA (additive, dominance, and additive x additive) model study showed the effects of additive gene action accounted for 54% of the phenotypic variance in lint percentage (Saha et al., 2010). Although environment affects fiber quality traits, genetic factors control much of the variation in fiber traits with additive variance being the strongest (Zhang, 2014)

Jenkins et al. (2012) reported genetic effects of CSL were mainly additive when top-crossed with elite upland cultivars. This study included CSL (CS-B4-15, CS-B10-19, CS-B 17-11, and CS-B 16-15) with whole or partial chromosome arms from two chromosomes. Jenkins et al. (2012) study reported the association of lint % with chromosome 10, 16-15, longer fibers with chromosome/arm 1, 11sh, 26Lo, uniformity with chromosome/arm 1, 11sh, 10, 17-11, stronger fibers with chromosome/arms 01, 11sh, 12sh, 26Lo, 10, 17-11, fiber elongation with chromosomes/arms 1, 11sh, 26Lo, 10, 17-11, and reduced fiber micronaire with chromosome/arms 1, 12sh, 4-15, 16-15, 17-11. The individual performances of CSL showed CS-B02, -04, -05sh, -06, -07, -15sh, and -22Lo with similar yield; In the same study, CS-B16, -18-, -05sh, -22sh, and -22Lo had higher lint percentage, CS-B25, -14sh, and -15sh had longer fibers, and CS-B02, -c25, -14sh, and -15sh had stronger fibers (Saha et al., 2004, 2006; Jenkins et al., 2007a, b).

CSL could be an advantage if crossed with other upland genotypes because a specific gene or a chromosomal segment can be targeted for an agronomic trait and/or a fiber quality trait. Moreover, only 3.8 percent (1 *barbadense* chromosome divided by a total number of 26 chromosomes) of non-*G. hirsutum* alleles are carried over by each CS-B line, thereby creating smaller amount of linkage drag. With more reliance on markers and marker-assisted selection (MAS), more QTLs affecting traits can be identified and screened early in the breeding populations. Development of markers and QTL mapping provide breeders with tools to make selections of desirable traits in the progeny in a shorter period of time (Saha et al., 2012).

Germplasm

TAM 182-33 (PI 654362), an extra long staple upland (ELSU), is a germplasm line developed by Texas A&M AgriLife Research and released in 2008 (Smith, 2009). Cotton Inc. identified ELSU as germplasm that exhibits an UHML equal to or exceeding 32 mm. TAM 182-33 was derived from the cross between two parental lines, TAM 94L-25 and PSC 161 (May et al., 1995). TAM 94L-25 (Smith, 2003) is a common parent among five families exhibiting the ELSU trait and was considered the progenitor of the ELSU trait. A performance trial that included TAM 182-33, under irrigated culture in 2007, reported the following agronomic and HVI fiber properties: lint yield of 911 kg ha^{-1}, 34 percent gin turnout, 4.1 mic, UHML 1.42 inches, 33.65 g tex^{-1} Str, 84.0 UI, and 3.3 percent elon (Smith et al., 2009).

TAM 06WE-621 (PI 671964) is an extra strength upland (ESU) germplasm line released in 2014 by Texas A&M AgriLife Research. One of the parents was the result of a cross between DP491 and TAM 96WD-18 (Thaxton et al., 2005; PI 635879), and the other parent was derived from the cross between TAM 91C-95Ls (Smith, 2001; PI 614952) and Deltapine Acala 90 (PVP 8100143) (Smith et al., 2014). Irrigated performance trials in 2009 and 2010 from Weslaco (Texas) reported the following HVI fiber properties: 921 kg ha^{-1} lint yield, 4.3 mic (2010), 1.20 inches UHML, 38.7 g tex^{-1} (2010), 85.0 UI, and 6.3% elon (Smith et al., 2014). It is yield competitive with cultivars grown in Central and South Texas while exhibiting larger and more seeds per boll when compared with a similar quality control cultivar, Acala 1517-08 (Smith et al., 2014).

Tamcot 73 (PI 662044) is an upland cotton cultivar developed by the Cotton Improvement Lab at Texas A&M AgriLife Research. It was derived from a complex series of crosses and was released in 2011. The HVI fiber properties, reported from the irrigated cultivar trials in four environments (2005-2007), are as follows: 38.5 lint percentage, 4.4 mic, 1.18 inches UHML, 31.8 g tex^{-1}, 84.3 UI, and 4.7 percent elon. Tamcot 73 produced the highest mean yield, 770 kg ha^{-1}, across all four dryland environments but was not significantly different than the commercial cultivars included in the 2009 cotton cultivar trials for central and south Texas. However, the lint % of TAMCOT 73 is not equivalent to commercial cultivars despite being a high yielding cultivar (Smith et al., 2009).

Mating Scheme

A line-by-tester method is used to screen for potential lines (germplasm or inbred lines) for the genetic improvement of their traits such as UHML in cotton. This particular method is utilized heavily in development of hybrids in maize (Narro et al., 2003; Nelson and Goodman, 2008; Bolduan et al., 2010; Badu-Apraku et al., 2011) and soybean (*Glycine max* L. Merr.) (Feng et al., 2004).

Breeders choose a set of testers that differ from each other for a variety of traits so that the genetic variability can be fully exploited and targeted. Therefore, the breeder must explore all crosses made among lines and testers in order to estimate the combining ability for a particular trait. A tester must be based on the following criteria: easy to use, allow for efficient screening of a line, and improve the trait of interest. The average

performance of the lines must be evaluated for it to be considered a good combiner for a trait (Hallauer et al., 2010).

General combining ability (GCA) is calculated for the lines and testers, and specific combining ability (SCA) is calculated for the F1 hybrids. A GCA estimate predicts the average performance of a line among the hybrids and is indicative of additive gene action. A SCA estimate defines the specific performance of an F1 hybrid among all the combined hybrids and is indicative of dominance or epistasis gene action (Hallauer et al., 2010). Breeders choose lines based on the estimated GCA and SCA estimates for the improvement of a trait of interest (Coyle and Smith, 1997).

This study's aim is to evaluate the potential of CSL in improving the UHML and Str of upland cotton as well as yield potential, by using LxT design. This project utilized 16 different CSL, three upland testers, and the original parents of the CSL. The 16 CSL with their two parents were crossed with three testers to create F_{1s}, which were grown in 2015 in a randomized complete block design. Fiber quality measurements were determined using HVI. GCA and SCA were determined for the lines, testers, and the F_{1s}. The LxT data could be of value for the improvement of UHML, Str, and yield potential by identifying beneficial alleles located on specific Pima chromosomes. The overarching goal of this study can be summarized into a basic question, "can we improve *G. hirsutum* elite materials for fiber quality traits and yield?"

The objectives of this research were –

1. **UHML** – Determine combining ability of the CSL for enhancing the extra long staple upland trait by utilization of an ELSU tester, TAM 182-33 ELSU.

2. **Str** – Determine combining ability of the CSL for enhancing the extra strength upland trait by utilization of an ESU tester, TAM 06WE-621.

3. **Yield -** Determine the combining ability of the CSL for fiber quality and yield by utilization of a high yielding, average fiber quality tester, TAMCOT 73.

CHAPTER III

MATERIALS AND METHODS

Breeding Material

Lines

The 16 CSL used herein were developed at the New Beasley Laboratory by Dr. David Stelly and Mr. Dwaine Raska at Texas A&M AgriLife Research, each with one G. *hirsutum* chromosome replaced by its homolog from G. *barbadense*, using modified recurrent backcrossing to a monosomic and monotelodisomic recurrent *G. hirsutum* parent and selection of the respective hypoaneuploid each BCnF1 generation. After identifying the hypoaneuploid BC5F1 hybrid, a euploid was identified among self-progeny and seed-increased. These experimental lines are identified herein as follows: CS-B01, CS-B02, CS-B04, CS-B05sh, CS-B06, CS-B07, CS-B11sh, CS-B12sh, CS-B14sh, CS-B15sh, CS-B16, CS-B17, CS-B18, CS-B22Lo, CS-B22sh, CS-B25. Each CSL is named for the chromosome that has been substituted. Parents of the CSL were TM-1 and 3-79. TM-1 (Kohel et al., 1970; PI 607172), an inbred of Deltapine 14, is a *Gossypium hirsutum*, while 3-79 is a photo-insensitive doubled haploid of *Gossypium barbadense.* These two parents were included as lines in the line x tester analysis. The total number of lines was eighteen.

Testers

The three testers were released by the Cotton Improvement Lab at Texas A&M. TAM B182-33 (PI 654362) ELSU exhibits an UHML exceeding 34.9 mm, and resulted

from a cross between TAM94L-25 and PSC 161. TAM 06WE-621 (PI 671964) is an ESU exhibiting a Str of approximately 38 g tex^{-1}, about 25 % greater than the best current commercial cotton cultivars. TAM 06WE-621 is a product of DP 491/TAM96WD-18//TAM91C-95Ls/DP Acala 90. Tamcot 73 (PI 662044), a product of complex series of crosses, was the third tester used in this study because of its high yield potential in central and south Texas.

Experimental Design

Breeding and Field Trial

In the summer of 2014, all CSL and corresponding parents were crossed with the three testers. A total of 54 crosses were made, 16 CSL plus TM-1 and 3-79 hybridized with each of the three testers. The crossing was located at the Texas A&M AgriLife Research Farm 300 near College Station, Texas. The crosses were made through hand-emasculation followed by hand-pollination. Each entry in the trial was self-pollinated to produce seeds for future use. A minimum of 20 pollinations were made per parental combination to ensure that enough seeds were produced for the LxT analysis.

During the summer of 2015, a total of 75 entries composed of F_1s, TM-1, 3-79, 16 CSL, and 3 testers were grown in a randomized complete block design at the Texas A&M AgriLife Research Farm in College Station, Texas with four reps of single-row 15-foot plots. The planting date was 11 May 2016 with additional emasculations and pollinations completed for testing in 2015. All 75 entries were self-pollinated. Thirty mature bolls were hand-harvested from each reps and ginned on a 10-saw laboratory gin.

Lint samples were evaluated at the Fiber and Biopolymer Research Institute at Texas Tech University for determination of HVI UHML, Micronaire, Str, UI, and Elon.

Each plot in 2015 consisted of 15 plants spaced 12 inches apart in a row with 40 inches being the between rows. The soil type was a Belk clay series, a Fine, Mixed, Thermic, Entic Hapluderts. Cultural practices were consistent with cotton production in central Texas, including furrow irrigation.

Statistical Analysis

Lint % was determined from hand-harvested boll samples as lint wt./seedcotton wt.*100. The analysis of variance was conducted for UHML, micronaire, Str, UI, elon, lint %, and seed cotton yield (scd) per hectare; however the emphasis of fiber quality will on UHML, Str, and yield. Mean squares were reported using SAS 9.4 (Cary, NC) Proc GLM for reps, genotypes (g), lines (l), testers (t), parents x crosses (p x c), and LxT.

Mean values were calculated for all 75 genotypes; Waller's LSD values were calculated for the mean values as $LSD = t_{.05, 60} * (2*ems/r)^{-½}$ and used for separating the mean values for all entries.

General combining ability (GCA) and specific combining ability (SCA) were calculated according to the formulas described in Falconer and McKay (1996).

$GCA_i = \mu_i - \mu$ is the formula used for calculating GCA estimates of the lines, where GCAi is the general combining ability of line i, μ_i is the mean of all hybrids with line i, and μ is the mean of all hybrids.

GCAj is the GCA value of the lines used against the testers. The formula is described as the following: $GCAj = \mu_j - \mu$. The GCAj is the general combining ability of tester j, μ_j is the mean of all hybrids with tester j, and μ is the mean of all hybrids.

SCA values were calculated according the following formula, $SCA_{ij} = \mu_{ij} – GCA_i – GCA_j – u$; where SCA_{ij} is the specific combining ability of line i with tester j, μ_{ij} is the mean value for line i with tester j, GCA_i is the calculated GCA of tester i, GCAj is the GCA value of line j, and μ is the mean of all hybrids.

The significance of SCA and GCA value were determined using a t-test at alpha= .05. The formula used for standard error calculation is described by Singh and Chaudhary (1985).

Standard errors for the GCA of lines were calculated as s.e. $(GCA_i) = \sqrt{MSE/(r \times t)}$, where MSE is the mean square of error, r is the number of replications and t is the number of testers. Standard error for GCA of testers was calculated as s.e. $(GCA_j) = \sqrt{MSE/(r \times l)}$, where MSE is the mean square of error, r is the number of replications and l is the number of lines. Standard error for SCA of LxT was calculated as s.e. $(SCA_{ij}) = \sqrt{MSE/r}$, where MSE is the mean square of error and r is the number of replications.

The performance above the MP value was calculated for a tester with the following equation: F_1 value – ((line + tester value)/2, where ‘line + tester value/2’ represented the mid-parent value. All the values were the phenotypic means of each genotype, which included lines, testers, and F_{1s}.

The estimates of genetic components were calculated as described in Kaushik et al. (1984). M values represent the mean square values determined in the analysis of

variance of line by tester analysis. For example, M_e represent the mean square value of error. The estimation values are based on usual least square theory. The variances were calculated according to the following formulas:

$\sigma^2 = M_e$ (Mean Sqaure value for error)

$\sigma^2 gca = (17\ (\sigma^2 line) + 2\ (\sigma^2 tester))/19$

$\sigma^2 sca = (M_{1xt} - M_e)/r$

$\sigma^2 line = (M_t - M_e)/r$

$\sigma^2 tester = (M_l - M_e)/r$

$\sigma^2 gca/\sigma^2 sca$ was calculated to determine the additive and/or dominance gene action. The $\sigma^2 gca$ includes degrees of freedom (numerical values) for lines and testers i.e., 17 and 2, respectively.

The Expected Mean Squares were calculated for Genotypes, Parents, Crosses, Lines, Testers, and Line x Tester under a fixed model effect.

	df	Expected Mean Square = EMS Fixed Model
Genotypes (g)	g-1	$\sigma^2_\varepsilon + r \sum \tilde{\lambda}^2_i /(g-1)$
Error	g (r-1)	σ^2_ε
Parents (p)	p-1	$\sigma^2_\varepsilon + r \sum \tilde{\lambda}^2_i /(p-1)$
Error	p (r-1)	σ^2_ε
Crosses (c)	c-1	$\sigma^2_\varepsilon + r \sum \tilde{\lambda}^2_i /(c-1)$
Error	c (r-1)	σ^2_ε

Lines (l)	l-1	$\sigma^2_\varepsilon + r \sum \alpha^2_i /(l-1)$
Testers (t)	t-1	$\sigma^2_\varepsilon + r \sum \beta^2_j /(t-1)$
Line x Tester (LxT)	(l-1)(t-1)	$\sigma^2_\varepsilon + r \sum (\alpha\beta)^2_{i,j} /(t-1)(l-1)$
Error	lt(r-1)	σ^2_ε

CHAPTER IV

RESULTS AND DISCUSSION

Analysis of Variance

Genotypes, including parents and crosses, varied significantly for HVI fiber properties (Table 1).

Table 1. Means squares for HVI fiber properties for genotypes, parents, and crosses grown at College Station, TX, in 2015

Source	df	Mic	UHML	UI	Str	Elon
Rep	3	0.560	0.023	10.5	8.59	33.0
Genotypes (g)	74	1.089**	0.034**	3.98**	26.4**	1.44**
Parents (p)	20	1.28**	0.03**	6.70**	42.8**	2.18**
Crosses (c)	53	1.03**	0.03**	2.09**	14.8**	0.75**
p vs. c	1	0.33	0.24**	49.6**	305.4**	22.9**
Error	219	0.31	0.08	64	17.9	61.1

*Significant at p<.05
**Significant at p<.01

When analyzed as a set of lines (CSL) and testers, significant differences were found among the CSL and among the three testers, although the interaction of lines with testers was not significant, despite significant difference among the F1 crosses (Table 2). These data indicate that the CSL responded the same to the three testers and that the three testers responded the same to the CSL. However, the phenotypic expressions of the CSL in this study are consistent with results reported by Saha et al. (2004).

Table 2. Means squares for HVI fiber properties for lines and testers grown at College Station, TX, in 2015

Source	df	Mic	UHML	UI	Str	Elon
Rep (Error A)	3	0.19	0.02	6.01	12.4	24.2
Lines (l)	17	2.60**	0.08**	4.61**	31.9**	1.44**
Testers (t)	2	4.30**	0.09**	7.22**	92.3**	2.49**
l x t	34	0.05	0.001	0.53	1.87	0.3
Error B	157	0.03	0.0006	0.54	1.46	0.24

*Significant at p<.05
**Significant at p<.01

Table 3. Means squares for Lint % and yield for genotypes, parents, and crosses grown at College Station, TX, in 2015

Source	df	Lint %	df	Yield (Scwt)
Rep	3	29.4	1	0.03
Genotypes (g)	74	28.8**	74	1.54**
Parents (p)	20	28.3**	20	1.28*
Crosses (c)	53	9.43**	53	0.876
p vs. c	1	297.08**	1	42.1**
Error	219	2.9	74	0.46

*Significant at p<.05
**Significant at p<.01

Genotypes, parents, crosses, and P vs C varied significantly in 2015 for Lint% while Genotypes, Parents, and P vs C varied significantly for scwt yield (Table 3). Contrary to the results of fiber properties (Table 1), yield was not significant among crosses, however parents and P vs C varied (p<.05). When lines and testers were

identified as sources of variation, the ANOVA, indicated no difference in yield for either lines or testers and no interaction (Table 4). However, the lines and testers varied for lint %. The lack of significance for yield may be due to extended rainfall that delayed harvest, caused shattering, and caused seed germination prior to harvest.

Table 4. Means squares for Lint % and yield for lines and testers grown at College Station, TX, in 2015

Source	df	Lint %	df	Yield (Scwt)
Rep	3	11.1	1	0.0006
Lines (l)	17	51.1**	17	0.98
Testers (t)	2	109.9**	2	2.46
l x t	34	2.5	34	0.73
Error	157	2.35	53	0.55

*Significant at p<.05
**Significant at p<.01

The primary focus of this research was the impact of the lines on the UHML of the testers, especially the ELSU tester, on the Str of the testers, especially the ESU tester, and yield of the testers, especially the high yielding Tamcot 73. However, HVI data were obtained for Mic, Elon, and UI that will be presented below as phenotypic descriptors of the CSL, testers, CSL parents, and crosses. These traits will not be discussed relative to the lxt analyses or combining ability.

The premium range for mic is 3.9 to 4.2 according to the USDA-AMS (USDA 2016). Five entries that exhibited mic within this premium range were CS-B17, TAM B182-33, TAM 06WE-621/CS-B25, TAM B182-33/CS-B01, and TAM B182-33/CS-B25 (Table 5). TAM B182-33/CS-B01 with a mic of 4.1 was not significantly different

than TAM B182-33/CS-B12sh that exhibited a mic of 4.4. However, the other four genotypes, CS-B17, TAM B182-33, TAM 06WE-621/CS-B25, and TAM B182-33/CS-B25, were significantly different from 67 of the total 75 genotypes. Of these four genotypes, two F_{1s} shared a common CSL i.e., CS-B25, which was significantly different than any of the other CSL/tester combinations ($p<.05$). This may suggest the presence of *G. barbadense* alleles on CS-B25 that code for desirable fiber diameter or fiber maturity when combined with other *G. hirsutum* genes on the other 25 chromosomes.

Line 3-79 exhibited a significantly high UI of 88.1% ($p<.05$), producing more than all of the genotypes (Table 5). The next best values were exhibited by TAM 06WE-621/3-79 and TAM B182-33/3-79, the interspecific crosses, at 87.7% and 87 %, respectively. TAM B182-33/CS-B25 exhibited an UI of 86.7% but was not significantly different than Tamcot 73/CS-B22Lo which exhibited an UI of 85.53%. With significant overlap among the genotypes especially among the F1s, it would be difficult to identify any chromosome as potential carriers of UI alleles.

Chromosome substitution lines CS-B17, CS-B01, CS-B04, and CS-B07 exhibited elon values of 8.4, 8.3, 8.3, and 7.9 respectively (Table 5). While CS-B07 was not significantly different than TAM 06WE-62-1/CS-B14sh which had an elon value of 7.63, the top three genotypes, i.e., CS-B17, CS-B01, and CS-B04, were significantly higher in elon values than TAM 06WE-62-1/CS-B14sh ($p<.05$). Numerically, 10 of 16 CSL exhibited an elon value higher than or equal to 7.0. CSL with higher elon values represented a deviation from its performance with other fiber quality parameters because

CSL performed poorly, on average (Table 5), for UHML, Str, mic, and UI among all the genotypes. Among all the crosses, Tamcot 73/CS-B01 exhibited the best elon at 7.48 but was not significantly different CS-B18 that exhibited an elon at. 6.94. No clear pattern emerged from the UI mean values where potential CSL could be explored for the presence of elon alleles.

Performance: Parents and Hybrids

UHML

Response to length tester

TAM B182-33/3-79 exhibited the longest ($p<.05$) UHML of 1.61 inches, 0.14 inches longer than its longer parent, 3-79. This high UHML was expected because it is an interspecific cross between *G. hirsutum* and *G. barbadense*. Tamcot 73/3-79 and TAM 06WE-62-1/3-79 were longer ($p<.05$) at 2nd place (1.54 and 1.55 inches, respectively) than all other crosses and parents with the exception of TAM B182-33/3-79. The *G. barbadense* parent, 3-79, of the CSL, exhibited a UHML of 1.47 inches, and the ELSU tester, TAM B182-33, exhibited a UHML of 1.37. A considerable amount of overlap was observed among the means of all the genotypes except for the interspecific crosses and 3-79. If only compared with other CSL, CS-B14sh exhibited the longest UHML at 1.25 inches, which is significantly shorter from the tester TAM B182-33 ELSU as well as 3-79. Of the 16 CSL crossed with tester TAM B182-33, 14 exhibited a UHML longer than longest CSL, CS-B14sh. Furthermore, the TAM B182-33/CS-B25 cross exhibited the longest UHML of 1.33 inches, an UHML longer than all other TAM

B182-33/CSL except TAM B182-33/CS-B14sh and TAM B182-33/CS-B16. This particular cross, i.e. TAM B182-33/CS-B25, was 0.30 inches lower in UHML than the interspecific cross of TAM B182-33 with 3-79. CS-B25 exhibited a longer ($p<.05$) UHML than all of the CSL except CS-B14sh.

Response to Str tester

Except for TAM 06WE-621/3-79 that exhibited a UHML of 1.55 inches, all other crosses with the high strength tester, TAM 06WE-621, produced significantly ($p<.05$) lower UHML values (Table 5). The interspecific cross was expected to produce a high UHML value since the *G. barbadense* parent of CSL, 3-79, carries superior fiber length alleles. The longest UHML among the Str tester crosses was exhibited by TAM 06WE-621/CS-B25 at 1.27 inches, which was significantly lower than the longest UHML using the length tester, i.e., TAM B182-33/CS-B25 at1.33 inches. However, this Str tester by CS-B25 produced a cross with an UHML longer than either parent, suggesting a good recombination or epistatic interaction(s). Six of the crosses of the 16 CSL with the Str tester produced UHML not different than the longest, TAM 06WE-621/CS-B25 at 1.27 inches.

Response to the yield tester

Crosses of the 16 CSL with Tamcot 73 resulted in numerically lower UHML in 14 combinations, numerically equal in one, and higher in one (Table 5). Tamcot 73/CS-B01 produced an UHML of 1.25 inches which was not significantly different than that

produced by this CSL when crossed with TAM B182-33 or TAM 06WE-621. This cross with CS-B01 was not longer than the cross of Tamcot 73 with CS-B-16 and all CSL crosses with Tamcot 73 were lower than the UHML of Tamcot 73/3-79, which was 1.54 inches. This again suggest that although the CSL may contain alleles for UHML, none of them individually contains a set of major genes that collectively favors high UHML or sufficient epistatic relationships that produces UHML approaching that obtainable with the full *G. barbadense* complement of alleles in 3-79.

Response across testers

Five CSL (CS-B14sh, CS-B15sh, CS-B16, CS-B17, and CS-B25) combined with all three testers to produce UHML significantly longer within each tester (Table 5). Within each tester there were exceptions to these five, e.g. CS-B07 with the length and strength testers, and CS-B01 with the yield tester. Regardless of the exceptions, these five CSL appear to harbor alleles that combine well with these testers for UHML.

Fiber Bundle Strength

Response to the Str tester

The high Str tester, TAM 06WE-621, produced the strongest HVI fiber bundle strength among all crosses and parents at 42.1 g tex^{-1}, significantly stronger than observed (40.4 g tex^{-1}) for 3-79, the CSL donor parent (Table 5). The cross exhibiting the highest Str was TAM 06WE-62-1/CS-B18 at 37.3 g tex^{-1} and this cross was not different than all of the remaining 15 TAM 06WE-621 crosses. This cross also is the

only CSL cross with TAM 06WE-621 that was not different greater than the CSL donor parent 3-79, 36.5 vs 37.3 g tex^{-1}. None of the CSL combined with the Str tester to produce fibers stronger than the tester parent which produced a Str of 42.1 g tex^{-1}. These data suggest that the 16 CSL, i.e., 16 of 26 *G. barbadense* chromosomes, do not possess alleles that would improve Str of the *hirsutum* tester, TAM 06WE-621. However, the cross of the high Str *G. hirsutum* tester with the *G. barbadense* CSL parent produced an F_1 with Str of 42.6 g tex^{-1}, which is stronger but not significantly different than TAM 06WE-621, but significantly stronger than 3-79, suggesting that alleles from the *G. hirsutum* tester improved the Str of the *G. barbadense* contribution.

Response to length tester

F1 hybrids from CSL crossed with TAM B182-33 exhibited significantly higher Str values than F1 hybrids from CSL crossed with other testers (Table 5). TAM B182-33/CS-B15sh exhibited the highest Str. i.e., 37.20 g tex^{-1}. Similar to the crosses with the Str tester, only two crosses failed to produce fibers stronger than the CSL parent, those being crosses with CS-B07 and CS-B18. Again suggesting that the most of the CSL did not provide alleles with dominance effects for Str when crossed with the length tester. Within the crosses with the length tester, TAM B182-33/CS-B15sh produced the strongest fibers at 37.2 g tex^{-1}, which was not different than TAM B182-33/CS-B18 and TAM B182-33/CS-B22sh. The CS-B18 and CS-B22sh also combined with the Str tester to produce the strongest fibers. These high Str values from a high length tester suggests that TAM B182-33 possesses beneficial alleles for high strength and high UHML. As

expected with the interspecific crosses, the TAM B182-33/3-79 F1 exhibited the highest Str at 39.5 g tex^{-1}, but was significantly lower ($p<.05$) than TAM 06WE-621 which exhibited the highest Str at 42.6g tex^{-1}.

Response to yield tester

Six CSL produced Str not different than the Str produced by their F_1 crosses with Tamcot 73, the yield tester (Table 5). All crosses with Tamcot 73 produces Str significantly lower than Tamcot 73, 36.0 g tex^{-1}. The numerally strongest fibers among the crosses with Tamcot 73 was with CS-B18, which was not different than Tamcot 73 crosses with CS-B11sh, B-22sh and B-25. Again, the cross of Tamcot 73 with the G. barbadense parent, 3-79, produced significantly stronger fibers at 40.9 g tex^{-1}, again suggesting that the 16 G. *barbadense* chromosomes in this study do not contain dominance effect alleles for Str or that the allelic interactions leading to G. *barbadense* Str are not intact on any of these specific chromosomes.

Response across testers

Phenotypically and based on parent and F_1 values, two CSL (CS-B18 and CS-B22sh) combined with the three testers to produce the strongest fibers within each tester (Table 5). Within each tester, there were exceptions, those being CS-B07 within the Str tester, CS-B15sh within the length tester, and CS-B11sh within the yield tester. Regardless of the exceptions, B18 and B22sh appear to have value in an applied breeding program for improving fiber bundle strength.

Lint %

Response to yield tester

The Cotton Improvement Lab has been challenged to produce elite fiber quality, especially UHML, within G. *hirsutum* that possesses commercial level lint % (pers. comm. C.W. Smith). Table 5 reveals this challenge with TAM B182-33, which possesses the ELSU trait, exhibiting a Lint % of 32.5 while TAM 06WE-621, the high strength tester, had a Lint % of 37.0 and Str of 42.1 g tex^{-1}, significantly higher than the 3-79 G. *barbadense* parent. The Tamcot 73 yield tester exhibited a relatively common but excellent fiber quality package and a Lint % of 38.4 g tex^{-1}.

Based on the Lint % phenotype of the CSL, CS-B22Lo should have produced the better Lint % in combination with the length tester, which exhibited a low Lint %. While that combination of TAM B182-33/CS-B22Lo produced Lint % better than nine of the 16 CSL combinations, it was not different than that produced with CS-B18, which exhibited a Lint % of only 26.0. These conflicting results suggest that Lint % is an extremely complex trait and probably controlled by complex and epistatic interactions that may conflict with those necessary for the ELSU trait. Certainly, within boll yield components such as fibers per unit seed surface area and lint density per seed logically would impact Lint % but the exact impact of longer fibers or stronger fibers is not apparent in the literature.

The cross of Tamcot 73 (high yield tester) and 3-79 produced a Lint % of 28.7, not different than the 3-79 parent and significantly lower than the Tamcot 73 parent

(Table 5). Tamcot 73/CS-B05sh produced a lint % of 28.5 which was not different than the 3-79 CSL *barbadense* parent. All other crosses of Tamcot 73 were significantly higher than 3-79 and Tamcot 73/3-79. However, none were higher than the Tamcot 73 tester, suggesting that the *barbadense* chromosomes involved in these CSL do not contribute alleles for improved Lint %. However, the cross Tamcot 73/CS-B02 produced a lint % of 39.6 which is not significantly different than the Tamcot 73 tester while all other crosses of Tamcot 73 were significantly lower, suggesting the loss of alleles for lint % by using the remaining 15 CSL. This result highlights the complexity of this trait because the CSL parent, CS-B02 had numerically the lowest Lint % of any CSL.

Response to Str and UHML tester

TAM 06WE-621/CS-B15sh exhibited a Lint % of 39.2 which was only 0.6% lower and not different than the highest lint % of 39.6 exhibited by Tamcot 73/CS-B02 noted above and in Table 5. The 3rd and 4th highest Lint % (numerically) were also exhibited by crosses with the Str tester, TAM 06WE-621, with CS-B16 (37.4%) and CS-B18 (37.1%) did not produce any lint % significantly better than as compared to the crosses made with TAM 06WE-621 and Tamcot 73. The CSL generally did not combine well with TAM B182-33 for Lint % with 12 of the 16 F_1 exhibiting Lint % lower than the best combination with TAM06WE-621. While Tamcot 73 was expected to provide alleles for Lint % when combined with the CSL, the data in Table 5 suggest that TAM 06WE-621, the strength tester, would be a better choice in a breeding program

for this trait. This conclusion is supported by the lack of difference between the highest Lint % producer, TAM 06WE-621/CS-B15sh, and the second highest producer TAM 06WE-621. Short arm of chromosome 15 could be presumed to possess favorable alleles for Str and Lint % as indicated by results in Table 5, but CSLCS-B15sh neither exhibits a high Str or Lint % when compared with other CSL and crosses, again highlighting the complexity of these traits in upland cotton.

Yield

Response to yield tester

Yield data among the genotypes included in this study are suspect given the large amount of rainfall during harvest in 2015 (data not shown). A second year of data will be collected in 2016 and should add clarity to any conclusions or comparisons based on 2015 data.

The high yield tester, Tamcot 73, outyielded the 3-79 CSL barbadense parent but was not different in seedcotton per acre than TAM B182-33, TAM 06WE-621, or TM-1 (Table 5). The highest seedcotton yield was observed with the cross of Tamcot 73/CS-B01 at 4928 lbs acre^{-1}, significantly higher than the three testers, the CSL parents, and all of the CSL in the study except CS-B07 and CS-B22Lo. However it was not higher yielding ($p=0.05$) than 11 other CSL crosses with Tamcot 73, 6 crosses with TAM B182-33, and 4 crosses with TAM 06WE-621. Of the two high yielding CSL, only the combination of CS-B22Lo and Tamcot 73 produced a yield numerically greater than the CSL. Crosses of the three testers used in the study with the CSL generally resulted in a

numerical improvement in the average yield of the CSL except in the case of CS-B07 and CS-B22Lo, the two high yielding CSL. Crosses of all three testers with CS-B07 averaged lower yield than the CSL parent and crosses of TAM 04WE-621 and TAM B182-33 with CS-B22Lo were lower yielding numerically than the CSL parent. Crossing the CSL with the yield tester, Tamcot 73, resulted in 7 of the 16 combinations producing significantly more seedcotton per acre than the CSL parent, while crosses with the length tester, B182-33, resulted in 8 of 16 higher yielding than there CSL parents and no cross with TAM 06WE-621 produced a higher yielding F_1. Obviously, the higher yielding the CSL then the lower the probability that a cross with any tester would result in significantly higher yield. If one considers only crosses with the yield tester, Tamcot 73, then potential CSL as parents for improving yield would include CS-B01, B02, B11sh, B14sh, B15sh, B16, B17, B18, and B22sh.

Response to Str and length tester

This study suggests four hybrids that performed well, when compared with all the other F_{1s} in their respective category of UHML, Str, lint %, and yield. TAM 183-33/CS-B25 (UHML) and TAM 06WE-6-21/CS-B18 (Str), while exhibiting the best numerical value for their respective category, failed to produce higher significant phenotypic means than their tester as well as the *barbadense* parent, 3-79.

Tamcot 73/CS-B02 (Lint %) was able to produce a significant Lint % value which may indicate the possession of beneficial alleles for chromosome 2 ($p<.05$).

Tamcot 73/CS-B01 (Yield) did yield the highest but was not significantly different than the next 25 genotypes in the experiment.

Table 5. Mean Values for HVI Fiber properties and yield potential of all genotypes grown at College Station in 2015

Entries	Mic	UHML (inches)	UI	Str (g tex^{-1})	Elon	Lint %	Scwt Yield (lbs $acre^{-1}$)
CS-B01	4.26	1.17	83.8	30.5	8.33	30.6	2363
CS-B02	5.12	1.11	82.4	31.3	5.88	25.4	1922
CS-B04	4.79	1.20	84.1	31.3	8.33	31.6	2961
CS-B05sh	5.24	1.11	83.0	29.3	6.85	34.6	2528
CS-B06	5.28	1.12	83.4	30.9	7.33	32.1	2689
CS-B07	5.23	1.16	84.4	33.1	7.93	32.9	4003
CS-B11sh	5.36	1.14	83.8	31.6	6.68	32.7	2516
CS-B12sh	5.10	1.13	83.9	31.1	7.00	32.6	2972
CS-B14sh	4.68	1.25	85.1	32.2	7.15	30.5	1807
CS-B15sh	4.93	1.17	84.2	33.4	7.20	32.1	2587
CS-B16	4.65	1.16	83.2	31.7	7.63	33.7	2151
CS-B17	4.10	1.16	83.9	32.0	8.45	27.9	2336
CS-B18	4.99	1.20	84.2	36.5	6.94	26.0	1495
CS-B22Lo	5.54	1.08	83.9	31.4	7.20	36.9	4020
CS-B22sh	4.89	1.06	83.5	32.1	7.23	33.4	2043
CS-B25	3.56	1.21	84.8	31.7	6.15	29.0	3108
TAM B182-33	3.91	1.37	86.8	37.0	6.18	32.5	2239
TAM 06WE-621	4.64	1.22	85.8	42.1	6.13	37.0	3203
Tamcot 73	5.01	1.23	85.2	36.0	7.00	38.4	2873
TM-1	4.81	1.19	85.1	32.2	7.23	31.3	2967
3-79	3.57	1.47	88.1	40.4	6.35	28.4	1355
TAM 06WE-621/CS-B01	4.49	1.22	85.4	35.3	7.20	35.8	3639
TAM 06WE-621/CS-B02	5.02	1.22	84.8	37.2	5.88	36.4	3976
TAM 06WE-621/CS-B04	4.62	1.23	85.3	36.6	6.83	36.4	3889
TAM 06WE-621/CS-B05sh	4.86	1.23	85.1	35.4	6.65	36.0	3168
TAM 06WE-621/CS-B06	5.04	1.22	84.7	35.3	6.43	35.8	4343
TAM 06WE-621/CS-B07	4.94	1.24	85.9	36.9	6.73	34.8	2807

Table 5. Continued

Entries	Mic	UHML (inches)	UI	Str (g tex^{-1})	Elon	Lint %	Scwt Yield (lbs acre^{-1})
TAM 06WE-621/CS-B11sh	4.90	1.23	85.6	35.9	6.35	36.3	3714
TAM 06WE-621/CS-B12sh	4.80	1.21	85.7	35.7	6.73	35.8	3281
TAM 06WE-621/CS-B14sh	4.90	1.24	85.9	36.2	7.00	35.3	3179
TAM 06WE-621/CS-B15sh	4.83	1.23	85.4	36.2	6.35	39.2	4053
TAM 06WE-621/CS-B16	5.16	1.24	84.9	36.3	6.53	37.4	3144
TAM 06WE-621/CS-B17	4.51	1.24	86.0	35.7	6.78	34.8	3412
TAM 06WE-621/CS-B18	5.06	1.21	85.2	37.3	6.58	37.1	3394
TAM 06WE-621/CS-B22Lo	5.19	1.19	85.4	36.1	6.55	36.9	3652
TAM 06WE-621/CS-B22sh	5.13	1.18	85.4	37.1	6.13	36.1	3619
TAM 06WE-621/CS-B25	4.20	1.27	86.2	35.3	6.10	34.0	3696
TAM 06WE-621/TM-1	4.98	1.26	85.9	39.1	5.45	36.1	3325
TAM 06WE-621/3-79	3.02	1.55	87.7	42.6	6.33	27.6	3926
TAM B182-33/CS-B01	4.07	1.27	85.4	33.7	6.70	32.9	2807
TAM B182-33/CS-B02	4.52	1.27	85.4	34.7	5.90	33.8	3375
TAM B182-33/CS-B04	4.47	1.27	85.0	34.1	6.70	34.8	3778
TAM B182-33/CS-B05sh	4.64	1.22	84.1	33.1	6.08	35.3	3815
TAM B182-33/CS-B06	4.57	1.25	85.3	35.1	6.10	34.0	3064
TAM B182-33/CS-B07	4.58	1.28	86.0	34.4	6.45	34.6	2806
TAM B182-33/CS-B11sh	4.66	1.27	85.3	34.1	6.58	33.8	3638
TAM B182-33/CS-B12sh	4.42	1.23	84.6	34.2	6.33	34.0	3281

Table 5. Continued

Entries	Mic	UHML (inches)	UI	Str (g tex^{-1})	Elon	Lint %	Scwt Yield (lbs acre^{-1})
TAM B182-33/CS-B14sh	4.54	1.30	85.6	34.8	6.38	32.3	2915
TAM B182-33/CS-B15sh	4.53	1.27	85.8	37.2	6.08	33.4	3809
TAM B182-33/CS-B16	4.51	1.31	85.2	34.9	6.38	32.7	3802
TAM B182-33/CS-B17	4.36	1.27	85.4	35.0	7.10	34.4	3860
TAM B182-33/CS-B18	4.93	1.22	84.3	36.1	5.78	35.9	2583
TAM B182-33/CS-B22Lo	4.86	1.22	85.1	34.6	6.08	35.3	2984
TAM B182-33/CS-B22sh	4.47	1.23	85.7	36.1	6.08	26.4	4329
TAM B182-33/CS-B25	3.92	1.33	86.7	34.8	6.85	32.0	3618
TAM B182-33/TM-1	4.24	1.32	85.3	37.2	6.00	32.9	2232
TAM B182-33/3-79	2.75	1.61	87.0	39.5	5.78	25.1	4504
Tamcot 73/CS-B01	4.70	1.25	85.3	33.9	7.48	35.5	4928
Tamcot 73/CS-B02	4.91	1.19	84.9	33.8	6.00	39.6	4302
Tamcot 73/CS-B04	4.92	1.22	84.9	33.2	7.05	35.2	3477
Tamcot 73/CS-B05sh	5.09	1.18	84.2	32.7	6.14	28.5	2658
Tamcot 73/CS-B06	4.83	1.18	84.5	32.8	6.23	35.9	3814
Tamcot 73/CS-B07	5.11	1.18	85.1	33.9	7.23	36.0	3145
Tamcot 73/CS-B11sh	5.08	1.19	85.1	34.6	6.33	36.7	4877
Tamcot 73/CS-B12sh	4.72	1.14	83.5	32.5	7.10	36.4	3803
Tamcot 73/CS-B14sh	5.05	1.20	84.9	33.7	6.60	35.4	3527
Tamcot 73/CS-B15sh	4.89	1.21	84.9	34.2	6.50	34.6	3813

Table 5. Continued

Entries	Mic	UHML (inches)	UI	Str (g tex^{-1})	Elon	Lint %	Scwt Yield (lbs acre^{-1})
Tamcot 73/CS-B16	4.99	1.24	84.8	33.6	6.83	36.1	4345
Tamcot 73/CS-B17	4.88	1.20	85.0	33.9	7.40	35.7	4055
Tamcot 73/CS-B18	5.26	1.19	84.2	35.9	6.25	36.7	4234
Tamcot 73/CS-B22Lo	5.24	1.18	85.5	34.7	6.95	36.6	4273
Tamcot 73/CS-B22sh	5.15	1.16	85.0	35.7	6.73	36.2	4306
Tamcot 73/CS-B25	4.53	1.21	85.7	34.4	6.33	34.4	3767
Tamcot 73/TM-1	4.87	1.24	85.2	35.5	6.25	35.1	3132
Tamcot 73/3-79	3.25	1.54	86.7	40.9	6.70	28.7	2865
LSD (.05%)	0.27	0.036	1.06	1.63	0.67	2.39	1184

General Combining Ability (GCA)

UHML

15 CSL were significant in their general combining ability for UHML across the three testers with the exception of CS-B14sh (Table 6). These results were expected given the lines each contain up to 3.8% alleles from a different species and the testers are phenotypically dissimilar. Although 15 of 16 CSL were significant, only two were significant with positive GCA estimates, which were CS-B16 and CS-B25. These CSL, CS-B16 and CS-B25, contributed .02 inches of UHML indicating the presence of UHML alleles in chromosomes 16 and 25. This assumption is affirmed by the results of the phenotypic means in table 5, where TAM B183-33/CS-B25 produced the longest UHML at 1.33 inches and TAM B182-33/CS-B16 produced a UHML at 1.31 inches

compared with all crosses. CS-B16 and CS-B25 averaged 1.16 inches and 1.21 inches (respectively), which were significantly lower than the TAM B182-33 length tester. This could suggest a favorable transfer of longer fiber alleles facilitated by these *barbadense* chromosome. TAM B182-33/CS-B25 did exhibit an UHML which was equal ($p=0.05$) to its tester TAM B182-33 but was lower than the *barbadense* parent, 3-79, of the CSL. This GCA estimate for TAM B182-33/CS-B25 is similar to that for 3-79 of 0.32 inches averaged across the three testers TM-1 exhibited a UHML GCA estimate of .02 inches, equivalent to the GCA estimates of CS-B25 and CS-B16. The negative GCA estimates for the remaining 13 CSL could suggests that the alleles located on these *barbadense* chromosomes have a negative impact on fiber length, either directly or through unfavorable epistatic interactions

GCA estimates for UHML were inconsistent with Jenkins et al. (2012) who showed the predicted additive effects of the arms/chromosomes of CS-B26Lo, CS-B01, and CS-B11sh as potential carriers of UHML alleles. The results of GCA estimates reported in this study suggested a zero and a significant negative estimate for CS-B01 and CS-B11sh, respectively, suggesting that they are not contributors of UHML alleles. The testers used in Jenkins et al. (2012) consisted of commercial cultivars and not elite quality experimental strains used in this study, which might suggest a different CSL to be significant than reported by Jenkins et al. (2012).

The GCA estimate of TAM B182-33 was not significant and unexpectedly low at .04 inches. This was unexpected since the tester chosen for the study was an ELSU, TAM 182-33, that exhibited an UHML at 1.37 inches (Table 5) and its UHML has been

reported as high as 1.44 inches (experimental data not shown). To better explain this discrepancy, the performance above MP is reported in Table 7. These data showed that TAM B182-33 hybrids with the 16 CSL produced UHMLs greater than the MP mean in eight of the 16 crosses. The best performers in UHML above the MP were crosses of the length tester with CS-B02 (0.03 inches), B16 (0.05 inches), and B25 0.04 inches).

Both of the other testers, TAM 06WE-621 and Tamcot 73, had negative and non-significant GCA estimates suggesting that they would not be good candidates as parents to improve UHML across these CSL (Table 6). However, if breeding value for UHML was based on performance above the MP value then TAM 04WE-621 was an excellent combiner with these CSL with values ranging from 0.00 to 0.7 inches (table 7). The MP values suggest that CSL CS-B02, B05sh, and B25 combined well with the strength tester for UHML. Tamcot 73 added UHML in 10 of the CSL with the best performance above MP value for crosses with CS-B01 and CS-B16 at .05 inches, although the GCA for Tamcot 73 in the LxT analysis was negative and non-significant. The GCA estimates, the value above MP, and the phenotypic evaluation suggest that CS-B16 and CS-B25 potentially were the best candidates among these CSL possessing alleles that contribute to UHML.

Table 6. Estimates of General Combining Ability (GCA) effects for UHML, Str, lint %, and Scwt Yield among lines and testers grown in College Station, TX, 2015.

	UHML (inches)	**Str (g tex^{-1})**	**Lint %**	**Scwt Yield (lbs acre^{-1})**
Lines	GCA	GCA	GCA	GCA
CS-B01	-0.001**	-1.14**	0.145**	473**

Table 6. Continued

	UHML	Str (g tex^{-1})	Lint %	Scwt Yield
CS-B02	-0.022**	-0.20**	1.99**	565**
CS-B04	-0.008**	-0.803**	0.840**	396**
CS-B05sh	-0.036**	-1.72**	-1.33**	-104
CS-B06	-0.033**	-1.05**	0.630**	421**
CS-B07	-0.015**	-0.362**	0.559**	-399**
CS-B11sh	-0.020**	-0.578**	0.972**	757**
CS-B12sh	-0.054**	-1.30**	0.788**	136
CS-B14sh	-0.002	-0.520**	-0.279**	-111**
CS-B15sh	-0.012**	0.413**	1.127**	573**
CS-B16	0.017**	-0.495**	0.795**	445**
CS-B17	-0.017**	-0.562**	0.384**	457**
CS-B18	-0.044**	1.02**	1.96**	85
CS-B22Lo	-0.055**	-0.295**	1.656**	317**
CS-B22sh	-0.057**	0.855**	-1.70**	766**
CS-B25	0.023**	-0.603**	-1.17**	375**
TM-1	0.020**	1.81**	0.086	-422**
3-79	0.317**	5.57**	-7.45**	446**
s.e.	0.002	0.081	0.102	99.1
	UHML (inches)	**Str (g tex^{-1})**	**Lint %**	**Scwt (lbs acre^{-1})**
Testers	GCA	GCA	GCA	GCA
TAM B182-33 elsu	0.037	-0.240	-1.63**	81**
TAM 06WE-62-1	-0.004	1.24**	1.04**	249**
Tamcot 73	-0.032	-1.00**	0.581	532**
s.e.	0.155	0.161	0.149	16.5
****significant at .05%**				

Fiber Bundle Strength

For Str, the calculated GCA estimates for the lines ranged from -1.720 g tex^{-1} for CS-B05sh to 1.020 for CS-B18 (Table 6). The largest GCA estimate was 5.57 g tex^{-1} for the CSL Pima parent 3-79 and even the *hirsutum* parent, TM-1, improved Str across all testers by an estimate of 1.8 g tex^{-1}. CS-B15sh, CS-B18, and CS-B22sh were three CSL that exhibited significant and positive GCA; all three combined with the testers to improve Str by .413 g tex^{-1}, 1.02 g tex^{-1}, and .855 g tex^{-1}, respectively, suggesting the presence of Str alleles on these *barbadense* chromosomes. This assumption is supported by the TAM 06WE-621/CS-B18 as well as CS-B18 which exhibited a high Str at 37.3 g tex^{-1} and 36.5 g tex^{-1}, respectively. However, this particular cross was significantly lower than TAM 06WE-621 as well as 3-79 (Table 5). CS-B22sh and CS-B15sh exhibited Str values similar to CS-B18 at 37.1 g tex^{-1} and 36.2 g tex^{-1}, respectively. These results could be used to identify chromosomes for high Str alleles in *barbadense* parent. Both parents, TM1 and 3-79, showed GCA estimates that were significant from zero (Table 6.). A significant GCA estimate at 5.6 g tex^{-1} was certainly expected from 3-79 because Pima cultivars contain high fiber strength alleles.

Jenkins et al. (2012) reported three CSL being significant and positive for Str: CS-B11sh and CS-B12sh. However, this study did not validate the Str CSL identified by Jenkins et al. (2012), suggesting that this could be due to the use of different tester(s) or an environment effect resulting from the different locations of the two studies.. The GCA estimates in table 6 suggest that CS-B11sh, CS-B12sh, and CS-B17 have a negative impact on Str, the opposite of Jenkins et al. across the testers used in this study.

As expected, the tester TAM 06WE-621 showed a significant GCA estimate value of 1.24 g tex^{-1} when combined with the 16 CSL, suggesting that TAM 06WE-621 contributed alleles for Str among the CSL (Table 6). However, since TAM 06WE-621 exhibited Str significantly greater than all other genotypes in the study, including the barbadense 3-79 (Table 5), most of the performance above MP shown in table 8 were negative, except for the MP values for CS-B02 at .54 g tex^{-1} and CS-B22sh at .02 g tex^{-1}. The GCA estimates showed that CSB-02 reduced strength by .20 g tex^{-1} but CS-B22sh increased Str by .855 g tex^{-1} when derived using all three testers. Considering both the CGA and the value above mid-parent suggest that CS-B22sh could have positive breeding value for Str.

The other testers, TAM B182-33 and Tamcot 73, exhibited negative GCA estimate of -0.24 g tex^{-1} (not significant) and -1.00 g tex^{-1} (significant), respectively, when crossed with the 16 CSL and their parents (Table 6). TAM B182-33 produced 6 negative and 10 positive MP performance values for Str across the 16 CSL, with crosses with CS-B15 and B22sh, two of the three CSL with positive and significant GCA, exceeding the MP values by 2 g tex^{-1} (Table 7). The TAM B182-33 cross with the other CSL with a significant and positive GCA, CS-B18, did not exceed the mid parent value. Thus B22sh appears to have breeding value relative to Str since it exhibited significant and positive GCA across the three testers and its F1 with TAM B182-33 and TAM 06WE-621 numerically exceeded the MP values for str. None of the Tamcot 73 tester crossed with the 16 CSL produced crosses that exceeded the MP value for Str which confirmed the negative GCA for this tester.

Table 7. Performace analysis of mid-parent value for each tester by a CSL for UHML, Str, Lint %, and Scwt Yield

		TAM B182-33		TAM 06WE-621		Tamcot 73	
Traits	**Lines**	**MP**	**P[1] above MP**	**MP**	**P above MP**	**MP**	**P above MP**
UHML (inches)	**CS-B01**	1.27	0.01	1.19	0.03	1.20	0.05
	CS-B02	1.24	0.03	1.16	0.06	1.17	0.02
	CS-B04	1.28	-0.01	1.21	0.03	1.21	0.01
	CS-B05sh	1.24	-0.02	1.16	0.07	1.17	0.01
	CS-B06	1.24	0.01	1.17	0.05	1.17	0.00
	CS-B07	1.26	0.02	1.19	0.05	1.19	-0.01
	CS-B11sh	1.25	0.02	1.18	0.05	1.18	0.01
	CS-B12sh	1.25	-0.02	1.17	0.04	1.18	-0.04
	CS-B14sh	1.31	-0.01	1.23	0.01	1.24	-0.04
	CS-B15sh	1.27	0.00	1.19	0.04	1.20	0.01
	CS-B16	1.26	0.05	1.19	0.05	1.19	0.05
	CS-B17	1.26	0.00	1.19	0.05	1.19	0.01
	CS-B18	1.28	-0.06	1.21	0.00	1.21	-0.03
	CS-B22Lo	1.22	-0.01	1.15	0.04	1.15	0.02
	CS-B22sh	1.21	0.02	1.14	0.04	1.14	0.02
	CS-B25	1.29	0.04	1.21	0.06	1.22	-0.01
	TM-1	1.28	0.04	1.20	0.05	1.21	0.03
	3-79	1.42	0.19	1.34	0.20	1.35	0.19
		TAM B182-33		**TAM 06WE-621**		**Tamcot 73**	
Tester	**Lines**	**MP**	**P above MP**	**MP**	**P above MP**	**MP**	**P above MP**
Str (g tex^{-1})	**CS-B01**	33.7	-0.05	36.3	-0.92	33.2	-2.15
	CS-B02	34.1	0.51	36.7	0.54	33.6	-2.18
	CS-B04	34.2	-0.11	36.7	-0.06	33.7	-2.83
	CS-B05sh	33.2	-0.02	35.7	-0.30	32.7	-3.28
	CS-B06	33.9	1.11	36.5	-1.19	33.4	-3.20
	CS-B07	35.1	-0.66	37.6	-0.69	34.6	-2.13
	CS-B11sh	34.3	-0.20	36.8	-0.90	33.8	-1.45
	CS-B12sh	34.1	0.15	36.6	-0.88	33.6	-3.55
	CS-B14sh	34.6	0.24	37.1	-0.91	34.1	-2.33

[1] Performance above Mid-Parent value

Table 7. Continued

	CS-B15sh	35.2	2.00	37.7	-1.58	34.7	-1.85
	CS-B16	34.4	0.51	36.9	-0.61	33.9	-2.38
	CS-B17	34.5	0.51	37.0	-1.36	34.0	-2.08
	CS-B18	36.7	-0.63	39.3	-1.93	36.2	-0.10
	CS-B22Lo	34.2	0.38	36.7	-0.60	33.7	-1.28
	CS-B22sh	34.6	1.57	37.1	0.02	34.1	-0.27
	CS-B25	34.4	0.39	36.9	-1.59	33.9	-1.60
	TM-1	34.6	2.58	37.1	1.93	34.1	-0.55
	3-79	38.7	0.84	41.2	1.34	38.2	4.90
		TAM B182-33		**TAM 06WE-621**		**Tamcot 73**	
Tester	**Lines**	**MP**	**P above MP**	**MP**	**P above MP**	**MP**	**P above MP**
Lint %	**CS-B01**	31.5	1.35	33.8	2.05	34.5	0.99
	CS-B02	29.0	4.86	31.2	5.14	31.9	7.69
	CS-B04	32.1	2.68	34.3	2.05	35.0	0.16
	CS-B05sh	33.5	1.79	35.8	0.21	36.5	-8.00
	CS-B06	32.3	1.75	34.5	1.23	35.2	0.62
	CS-B07	32.7	1.97	34.9	-0.09	35.6	0.35
	CS-B11sh	32.6	1.15	34.9	1.41	35.6	1.11
	CS-B12sh	32.5	1.42	34.8	1.01	35.5	0.92
	CS-B14sh	31.5	0.76	33.8	1.50	34.5	0.95
	CS-B15sh	32.3	1.07	34.6	4.65	35.3	-0.64
	CS-B16	33.1	-0.43	35.3	2.09	36.0	0.06
	CS-B17	30.2	4.24	32.4	2.32	33.1	2.59
	CS-B18	29.2	6.71	31.5	5.59	32.2	4.51
	CS-B22Lo	34.7	0.56	37.0	-0.04	37.7	-1.06
	CS-B22sh	32.9	-6.54	35.2	0.89	35.9	0.35
	CS-B25	30.8	1.20	33.0	0.95	33.7	0.63
	TM-1	31.9	0.98	34.2	1.89	34.9	0.23
	3-79	30.4	-5.38	32.7	-5.05	33.4	-4.65
		TAM B182-33		**TAM 06WE-621**		**Tamcot 73**	
Tester	**Lines**	**MP**	**P above MP**	**MP**	**P above MP**	**MP**	**P above MP**
Scwt Yield (lbs acre^{-1})	**CS-B01**	2301	506	2783	857	2618	2310
	CS-B02	2081	1294	2563	1413	2398	1904

Table 7. Continued

CS-B04	2600	1178	3082	807	2917	560
CS-B05sh	2384	1432	2866	303	2701	-42
CS-B06	2464	600	2946	1397	2781	1033
CS-B07	3121	-315	3603	-796	3438	-293
CS-B11sh	2378	1261	2860	854	2695	2182
CS-B12sh	2605	676	3087	194	2922	880
CS-B14sh	2023	892	2505	674	2340	1186
CS-B15sh	2413	1396	2895	1158	2730	1082
CS-B16	2195	1607	2677	467	2512	1833
CS-B17	2288	1572	2770	642	2605	1450
CS-B18	1867	716	2349	1045	2184	2050
CS-B22Lo	3130	-145	3612	40	3447	826
CS-B22sh	2141	2188	2623	996	2458	1848
CS-B25	2674	944	3156	540	2991	776
TM-1	2603	-370	3085	240	2920	211
3-79	1797	2707	2279	1647	2114	751

Lint %

The combining ability analysis for Lint % indicated a significant GCA estimates among the lines, testers and 3-79 but not TM-1 (Table 6). The GCA estimates ranged from -1.70 % for CS-B22sh to 1.99 % of CS-B02. Twelve of the 16 CSL exhibited a GCA value when crossed with the three testers that were positive as well as significantly different from zero. CS-B02 exhibited the highest Lint % GCA estimate of 1.99 % and with CS-B18 at 2nd highest of 1.96%, with CS-B22Lo at 3rd highest at 1.66%, suggesting the presence of Lint % alleles these chromosomes. Table 5 showed that CS-B02, when crossed with Tamcot 73, produced the highest significant value for lint %, i.e., 39.6 %, which supported the highest GCA estimate exhibited by CS-B02 at 1.99%. As a CSL, CS-B02 exhibited a significantly lower phenotypic mean Lint% at 25.4 indicating the

addition of Lint % alleles or epistatic interactions were mainly due to the tester, Tamcot 73. CS-B15sh exhibited the 4th highest GCA estimate at 1.13%, but it produced a Lint % at 39.2 when combined with TAM 06WE-621. This value is significantly equivalent to the highest producing Lint % value of 39.6 %, which was exhibited by Tamcot 73/CS-B02. As expected, the GCA estimate for the *G. barbadense* parent of CSL, 3-79 produced a highly significant but a negative GCA estimate indicating its ability to reduce Lint % by 7.46 % if used in an interspecific cross. These data confirm the complexity of Lint % and suggest that *G. barbadense* alleles on individual chromosomes may have positive effects on lint percent whereas crossing with a *G. barbadense* parent such as 3-79 brings in an overwhelming number of unfavorable alleles or creates an overwhelming negative epistatic effect on this trait.

Jenkins et al. (2006) observed CS-B18 to be non-significant, whereas the CS-B02 was significant but with a negative value for Lint %. The observations of Jenkins et al. (2006) is in disagreement with the results of this study which found CS-B02 as the best candidate for carrying potential Lint % alleles. The difference in results was probably due to the use of Tamcot 73 as the high yield tester in this study. In the present study, the Lint % GCA estimates of CSL predicts CS-B02 and CS-B18 as the best general combiners for Lint %.

As a tester, Tamcot 73 was not significant general combiner for increasing the Lint % of these CSL (Table 6). This was unexpected as since Tamcot 73 was included specifically for its agronomic profile. However, crosses of Tamcot 73 with 11 of the 16 CSL produced values above the MP less than 1 % with three of the F1s exhibiting Lint

% below the MP value. Tamcot 73/ CS-B05sh produced a Lint % that was 8.0 % below the MP; however Tamcot 73/CS-B02 produced a Lint % that was 7.7 % above the mid-parent (Table 7).

TAM 06WE-621 showed a significant and positive GCA estimate at 1.04 % when combined with the CSL and their parents in this study (Table 6). Based on values above the MP, TAM 06WE-621 performed well with CS-B18, B02, and B15sh by producing the values above the MP of 5.6 %, 5.1, and 4.7%, respectively. The MP performance values are supported by the mean values exhibited by TAM 06WE-621/CS-B18 at 37.1%, TAM 06WE-621/CS-B02 at 36.4 %, and TAM 06WE-621/CS-B15sh at 39.2%, (table 5). ‘

TAM B182-33 exhibited a negative and significant GCA for Lint % of -1.63 (Table 6). However, due to the low Lint % of the TAM B182-33 parent, 14 of the 16 crosses with this tester produced Lint % values exceeding the MP value (Table 7). These data indicate that the CSL, with the possible exceptions of CS-B16 and CS-B22sh, contributed alleles that improved Lint %. The F1 performance of TAM B182-33/CS-B18 was 6.7% above the MP, suggesting that this *G. barbadense* chromosome may contribute positive alleles for Lint %, although its parental Lint % was numerically one of the lowest in this test at only 25% (Table 5).

Based on GCA and values above the MP, CSL CS-B02 and CS-B18 seem to be excellent CSL candidates for improving Lint % in the CIL germplasm, including germplasm with the ELSU trait, the ESU trait, and yield potential (Tables 6, and 7)

Yield

The GCA estimates for yield are shown in Table 6. GCA estimates for Lines CS-B05sh, CS-B12sh, and CS-B18 were insignificant while the GCA estimates for CS-B07 and B-14sh were significant but negative. CS-B22sh produced the highest GCA estimate at 766 lbs acre^{-1} with the second highest exhibited by CS-B11sh at 757 lbs acre^{-1}. Three additional good GCA CSL were CS-B01, B02, and B15sh, all exhibiting a GCA effect of near 500 lbs/ac. The yield GCA estimate of 3-79 was an anomaly in these GCA data since 3-79 is not known for its high yield in College Station, TX.

Jenkins et al. (2006; 2012) identified CS-22sh and CS-22Lo as the potential carriers of alleles for yield because of their significant additive effects in yield potential. The results of this study indicate CS-B22sh as the best general combiner for yield, which is in agreement with the results of Jenkins et al. (2006) (Table 6). CS-B22Lo in this study agreed with the conclusion of Jenkins et al. (2006) but other CSL in our study exhibited better GCA than B22Lo.

Among the testers, Tamcot 73, as expected, was a good combiner for yield exhibiting a significant positive value of 532 lb/ac. (Table 6). The other two testers, Tam B182-33 and TAM 06WE-621, exhibited positive and significant GCA when crossed with this set of CSL. The value above MP data in Table 7 confirm the GCA estimates for the testers in that most crosses produced F1s with yield exceeding the MP value within each of the tester parents. The exceptions were when the three testers were crossed with CS-B07 or B22Lo, both of which exhibited yields among the highest across the Lines and Testers (Table 5). None of the F1 crosses between the testers and B07 exceeded the

MP value and the F1 of TAM B182-33/CS-B22Lo was lower yielding than the MP. The MP data confirm the GCA estimates that all three testers combined with the CSL for improved yield in the F1s, i.e., the testers contributed yield potential alleles when combined with these CSL; the possible general exception being CS-B07. It would be speculative to draw conclusions from the high value of yield GCA estimates since yield was collected from two reps for one year. Yield is a quantitative trait affected by a strong genotype x environment interaction.

Specific Combining Ability

The specific combining ability represents deviations from general combining ability, and is due to dominance genetic variance or epistatic interaction of alleles. It looks at the performance of specific parental combinations, but is used mainly in hybrid crops. The SCA estimates for the 54 hybrids are shown in Table 8.

UHML- Among the estimates for UHML from all the crosses, only 16 of the SCA estimates were significantly different than zero, with seven positive estimates and 9 negative estimates. Tamcot 73/CS-B01 exhibiting the highest SCA estimate at .035 inches. Tamcot 73/CS-B01 is a deviation from the results reported in Table 6 which showed CS-B01 with a UHML GCA of 0.0 and Tamcot 73 with a negative GCA at -.03 inches ($p<.05$). The second best SCA estimate was exhibited by TAM B182-33/CS-B25 at .025 inches which supported CS-B25 as the best general combiner. There was not a pattern of SCA relative to any specific tester, with seven significant specific

combinations, both positive and negative, with Tamcot 73, four with TAM 06WE-621, and five with TAM B182-33.

In terms of Str, only 4 out of 48 crosses among the three testers and 16 CSL exhibited significant SCA estimates with three being positive and one negative (Table 8). TAM B182-33/CS-B06 and Tamcot 73/CS-B18 produced SCA estimates of .915 g tex^{-1} and .458 g tex-1, respectively. Tamcot 73/CS-B18 did support CS-B18, as shown in the GCA table, as the best combiner for Str among all the CSL. The SCA of TAM B182-33/CS-B06 was a positive estimate although both parents exhibited significant and negative GCA estimates. Two specific combinations, TAM 06WE-621/CS-B15sh and TAM B182-33/3-79, exhibited negative SCA.

For Lint %, all the SCA estimates for crosses among the Testers, CSL, and the CSL parents were not significant (Table 8).

For yield, only two of the 14 significant SCA estimates were positive. TAM B182-33/3-79 cross exhibited the highest significant SCA value of 656 lbs $acre^{-1}$ followed by Tamcot 73/CS-B01 at 606 lbs $acre^{-1}$. TAM B182-33/3-79 is an anomaly because neither its tester nor the CSL are known for their high yield potential. Tamcot 73/CS-B01's SCA value is in agreement with the mean values provided in Table 5 that showed Tamcot 73/CS-B01 with the highest yield among all the F_{1s} and parental entries. CS-B01 did have a positive and significant GCA value, but it was not the best combiner for yield as shown in table 6. However, Tamcot 73/CS-B01 had the 2^{nd} highest SCA value in yield and the best SCA estimate in UHML, thereby suggesting it to be a good specific combiner.

Table 8. Estimates of Specific Combining Ability (GCA) effects for UHML, Str, lint % and yield among lines and testers grown in College Station, TX, 2015.

Crosses	UHML (inches)	Str (g tex^{-1})	Lint %	Scwt Yield (lbs acre^{-1})
TAM 06WE-62-1/CS-B01	-0.023**	-0.198	-0.023	-401
TAM 06WE-62-1/CS-B02	-0.002	0.735	-0.002	-157
TAM 06WE-62-1/CS-B04	-0.003	0.768	-0.003	-74
TAM 06WE-62-1/CS-B05sh	0.022**	0.435	0.022	-295
TAM 06WE-62-1/CS-B06	0.009	-0.340	0.009	353
TAM 06WE-62-1/CS-B07	0.006	0.602	0.006	-362
TAM 06WE-62-1/CS-B11sh	0.001	-0.182	0.001	-611**
TAM 06WE-62-1/CS-B12sh	0.020**	0.343	0.020	-423
TAM 06WE-62-1/CS-B14sh	-0.002	0.060	-0.002	-277
TAM 06WE-62-1/CS-B15sh	-0.002	-0.923**	-0.002	-88**
TAM 06WE-62-1/CS-B16	-0.018**	0.110	-0.018	-869**
TAM 06WE-62-1/CS-B17	0.008	-0.448	0.008	-612**
TAM 06WE-62-1/CS-B18	0.010	-0.357	0.010	-259
TAM 06WE-62-1/CS-B22Lo	0.001	-0.265	0.001	-233
TAM 06WE-62-1/CS-B22sh	-0.010	-0.415	-0.010	-715**
TAM 06WE-62-1/CS-B25	0.001	-0.757	0.001	-247
TAM 06WE-62-1/TM-1	-0.009	0.585	-0.009	179
TAM 06WE-62-1/3-79	-0.013	0.318	-0.013	-88
TAM B182-33/CS-B01	-0.012	-0.368	-0.012	-1066**
TAM B182-33/CS-B02	0.004	-0.335	0.004	-590
TAM B182-33/CS-B04	-0.007	-0.327	-0.007	-18
TAM B182-33/CS-B05sh	-0.026**	-0.335	-0.026	519
TAM B182-33/CS-B06	-0.002	0.915**	-0.002	-758
TAM B182-33/CS-B07	0.012	-0.418	0.012	-195
TAM B182-33/CS-B11sh	0.002	-0.527	0.002	-519
TAM B182-33/CS-B12sh	0.002	0.323	0.002	-255
TAM B182-33/CS-B14sh	0.017**	0.165	0.017	-373
TAM B182-33/CS-B15sh	-0.006	1.607**	-0.006	-164
TAM B182-33/CS-B16	0.011	0.190	0.011	-43
TAM B182-33/CS-B17	-0.003	0.382	-0.003	2
TAM B182-33/CS-B18	-0.023**	-0.102	-0.023	-902**
TAM B182-33/CS-B22Lo	-0.015**	-0.335	-0.015	-733**
TAM B182-33/CS-B22sh	0.009	-0.035	0.009	162
TAM B182-33/CS-B25	0.025**	0.173	0.025	-157
TAM B182-33/TM-1	0.010	0.190	0.010	-745**
TAM B182-33/3-79	0.005	-1.227**	0.005	656**
Tamcot 73/CS-B01	0.035**	0.567	0.035	603**
Tamcot 73/CS-B02	-0.002	-0.400	-0.002	-115

Table 8. Continued

Crosses	UHML (inches)	Str (g tex^{-1})	Lint %	Scwt Yield (lbs acre^{-1})
Tamcot 73/CS-B04	0.010	-0.442	0.010	-770**
Tamcot 73/CS-B05sh	0.004	-0.100	0.004	-1088**
Tamcot 73/CS-B06	-0.008	-0.575	-0.008	-458
Tamcot 73/CS-B07	-0.019**	-0.183	-0.019	-306
Tamcot 73/CS-B11sh	-0.004	0.708	-0.004	268
Tamcot 73/CS-B12sh	-0.022**	-0.667	-0.022	-184
Tamcot 73/CS-B14sh	-0.014**	-0.225	-0.014	-213
Tamcot 73/CS-B15sh	0.008	-0.683	0.008	-611**
Tamcot 73/CS-B16	0.007	-0.300	0.007	48
Tamcot 73/CS-B17	-0.004	0.067	-0.004	-253
Tamcot 73/CS-B18	0.013**	0.458**	0.013	298
Tamcot 73/CS-B22Lo	0.014**	0.600	0.014	103
Tamcot 73/CS-B22sh	0.001	0.450	0.001	-311
Tamcot 73/CS-B25	-0.026**	0.583	-0.026	-458
Tamcot 73/TM-1	-0.001	-0.775	-0.001	-297
Tamcot 73/3-79	0.007	0.908	0.007	-1432**
s.e.	.0065	0.4148	.4258	297
****Significant at .05%**				

Genetic Effects

The estimates of genetic components can be found in Table 9. The ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ for UHML, Str, and Lint % suggested additive gene action. Lint % had a larger additive effect compared with UHML and Str. These results seem to be supportive of studies reported by Jenkins et al., (2012) and Saha et al., (2010). The ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ for yield showed a value less than 1, thereby suggesting dominance gene action in yield

Table 9. Estimates of Genetic Components for UHML, Str, lint %, and yield.

	UHML	Str	Lint %	Yield
σ^2	0.0006	1.460	2.350	0.5500
σ^2_{gca}	0.0018	1.396	1.764	-0.0103
σ^2_{sca}	0.0001	0.1025	0.0375	-0.0900
σ^2_{line}	0.0012	1.262	1.494	-0.0031
σ^2_{tester}	0.0066	2.537	4.063	-0.0717
$\sigma^2_{gca}/\sigma^2_{sca}$	18.07	13.62	47.04	0.1142

For future research, the F2 generation will be tested and analyzed for phenotypic variation and then will be selected for selection of markers and detection of QTLs. Moreover, the four best GCA values exhibited by each CSL and tester combination (Table 6), will be used in development of recombinant inbred line populations. If a lack of significance is seen in an LxT analysis, perhaps a different set of testers can be used to screen for more chromosome/arms that may suggest the presence or the lack of beneficial alleles for fiber quality improvement. This study is a step forward in utilizing novel breeding techniques for introgressing fiber quality traits from *G. barbadense* into *G. hirsutum*.

CHAPTER V

CONCLUSION

The objective of this study was to use an LxT design to screen CSL for combining ability for UHML, Str, and yield potential. CS-B25 was the best in general combining ability for UHML at .023 inches. For Str, CS-B18 was the best general combiner for strength at 1.02 g tex^{-1}. In terms of yield properties, CSB-02 was highly significant and added about 1.99% of value in the category of Lint %. CS-B22sh was the best general combiner for yield potential. Therefore, the results of this study suggested four CSL for general combining ability in UHML (CS-B25), Str (CS-B18) CS-B02 (lint %) and CS-B11sh (yield).

Tamcot 73/CS-B01 was the best specific combiner for UHML and Scwt yield among all the F_{1s}. UHML, Str, and Lint % expressed additive gene action, whereas yield showed more dominance gene action.

This study will be expanded for future study by testing the best four hybrid combinations that out produced all other F_{1s} grown in our randomized complete block design. These four hybrids were chosen based on the phenotypic mean performance in UHML, Str, lint %, and yield

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